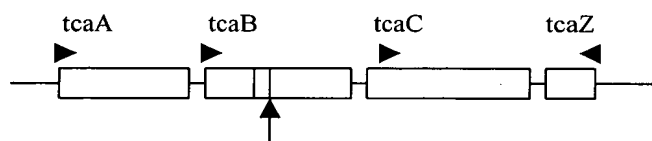
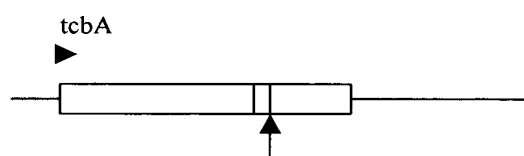


Photorhabdus

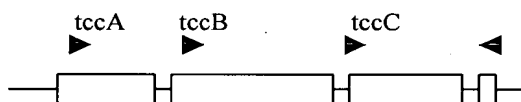
tca



tcb



tcc



tcd

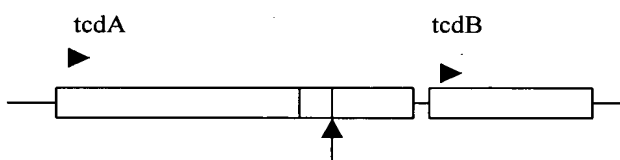


FIG. 1

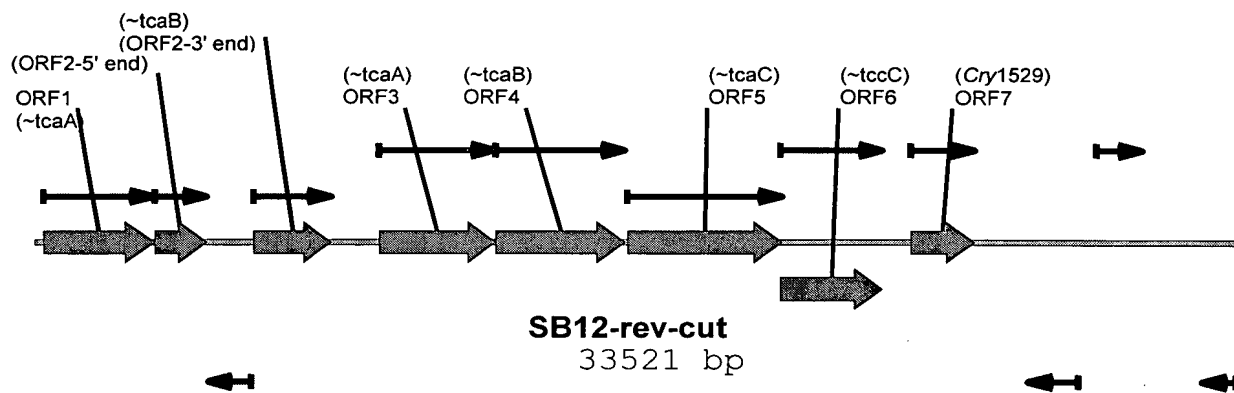


Fig. 2

2THIA

or

AAC44156: DITLKVAIYPYVPDPA RFQA

|||||

SEQ ID NO:17: DITLKVAIYPYVPDPS RFQA

Fig. 3

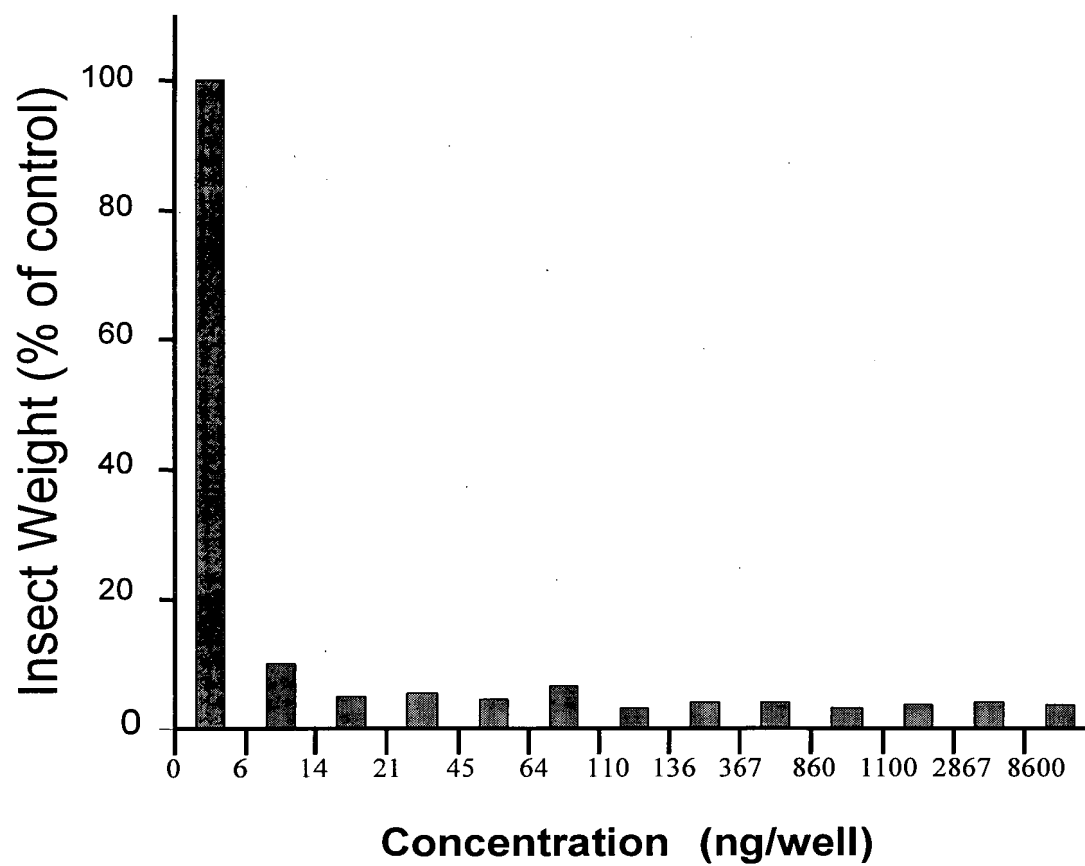


Fig. 4

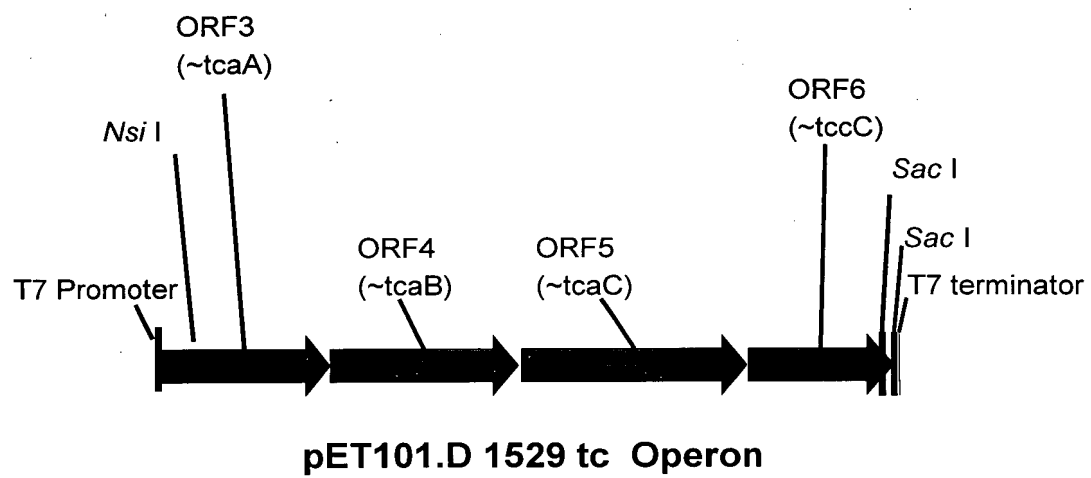


Fig. 5

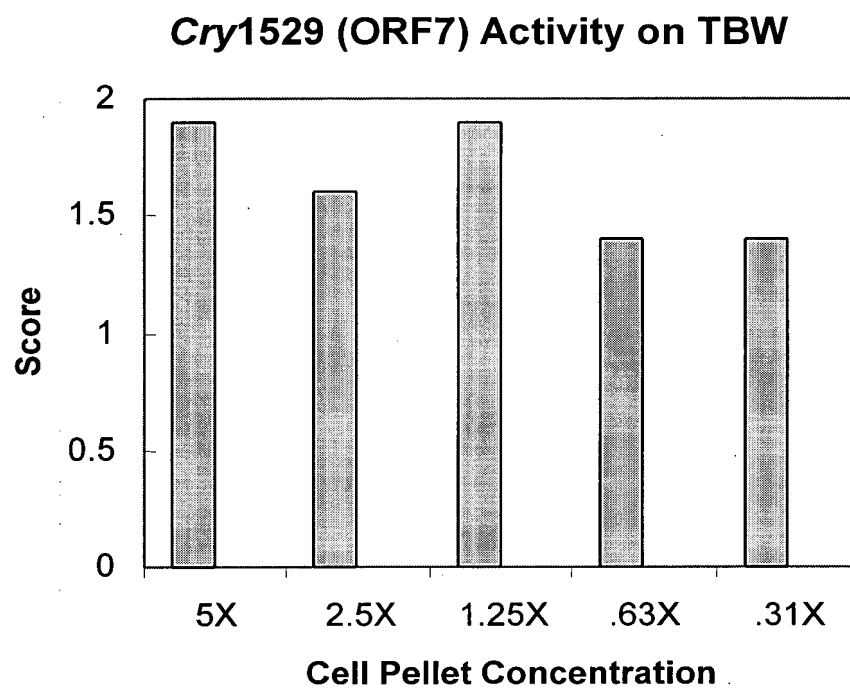


Fig. 6

```

      SEQ ID NO:9(top) x SEQ ID NO:5(bottom)
1  MTKEGDKHMSTSTLLQSIKEARRDALVNHYIANQVPTALADKITDADSLY 50
   |||||:|:||||||| || ||||| || ||||| |||||
1  MTKEGGKNMSTSTLLQLIKESRRDALVNHYIANNVPRELTDKITDADSLY 50
   |||||:|:||||||| || ||||| || ||||| |||||
51 EYLLLDTKISELVKTSPIAEAISSVQLYMNRCVEGYEGKLTPESENTHFGP 100
   |||||:|:||||||| || ||||| || ||||| |||||
51 EYLLLDTKISELVKTSPIAEAISSVQLYMNRCVEGYEGKLTPEGNSHFGP 100
   |||||:|:||||||| || ||||| || ||||| |||||
101 GKFLYNWDTYNKRFTWAGKERLKYAGSYIEPSLRYNKTDPFNLNEQSI 150
   ||||:||||||| ||||| ||||| ||||| ||||| |||||
101 GKFLNNWDTYNKRYSTWAGKERLKYAGSYIDPSLRYNKTDPFNLNEQNI 150
   ||||:||||||| ||||| ||||| ||||| ||||| |||||
151 SQGRITDDTVKNALQHLYLTEYEVVLADLDYISVNKGGDESVLFFVGRKTKV 200
   |||||:||||||| ||||| ||||| ||||| |||||
151 SQGRITDDTVKNALQHLYLTEYEVVLADLEYISVNKGADSVLFFVGRKTKM 200
   |||||:||||||| ||||| ||||| ||||| |||||
201 PYEYYWRRLLLKRDNNNKLVPVWSQWKKISANIGEAVDSYVVRWHKNR 250
   |||||:||||||| ||||| ||||| ||||| ||||| |||||
201 PYEYYWRRLTLKKNNNKLVPVWSQWKKITANIGEAVNNYVVLHWHNNR 250
   |||||:||||||| ||||| ||||| ||||| ||||| |||||
251 LHVQWCSIEKSENDAGEPIEKRYLNDWFMDSSGVWSSFRKIPVVEKSFEY 300
   ||||| || || ||:||||||| ||||| ||||| ||||| |||||
251 LHVQWGSTEKTQNDGGEPIEKRYLNDWFMDKSSVWSSFRKVSYIENSFTY 300
   ||||| || || ||:||||||| ||||| ||||| ||||| |||||
301 LDGSLDPRFVALVRNQILIDEPEIFRITVSAPNPIDANGRVEVHFEENYA 350
   | | | :|| | | :| | | | | :| :| :|
301 TEGIIDSRNITIAGNQLFCDDSNFTKATITA.LPFDQIRVYLEKIYGTGG 349
   | | | :|| | | :| | | | | :| :| :|
351 NRYNITIKYGTTSIAIPAGQVGHPNISINETLRVEFGTRPDWYYTFRYLG 400
   : : : :|| :| :| :| :| :| :| :| :|
350 SITVTGENKGYIIKVGEPREVSFSPNTLLDVFIGSNASPRDPYFKATFNR 399
   | | | :|| | | :| | | | | :| :| :|
401 NTIQNSYGSIVNNQFSPPSGSNIKGPIDLTLKNNIDLSALLDESLDALFD 450
   |||||: || ||||| ||||| ||||| ||||| |||||
400 EALQNSYGSIKINQYTPPSGSNIKGPIDLTLKNNIDLSALLEESLDVLF 449
   |||||: || ||||| ||||| ||||| ||||| |||||
451 YTIQGDNQLGGLAAFNGPYGLYLWEIFFHVPFLMAVRFHTE--QRYELAERW 500
   |||||:||||||| ||||| ||||| ||||| ||||| |||||
450 YTIQGNQLGGLAAFNGPYGLYLWEIFLHVPFLMAVRFHTE][QRYELAERW 499
   |||||:||||||| ||||| ||||| ||||| ||||| |||||
501 FKFIFNSAGYRDDYGSLLTDDKGNVRYWNVIPLOQEDTEWDDTSLATTD 550
   |||||:||||||| ||||| ||||| ||||| ||||| |||||
500 FKFIFNSAGYRDGYGNLLTDDKGNVRYWNVVPLQEDTEWDDTSLATTD 549
   |||||:||||||| ||||| ||||| ||||| ||||| |||||
551 DEIAMADPMQYKLAIFIHTMDFLISRGDSLYRMLERDTLAEAKMYIIQAS 600
   |||||:||||||| ||||| ||||| ||||| ||||| |||||
550 DEIAMADPMQYKLAIFIHTLDFLISRGDSLYRMLERDTLTEAKMYIIQAS 599
   |||||:||||||| ||||| ||||| ||||| ||||| |||||
601 QLLGPRPDIRLNHSWPNPTLQSEADAVTAVPTRSDSPAAPILALRALLTG 650
   ||||| || ||||| ||||| ||||| ||||| ||||| |||||
600 QLLGPRPEIRINHSWPDPTLQSEADAVTAVPTRSDSPAAPILALRALLNA 649
   ||||| || ||||| ||||| ||||| ||||| ||||| |||||

```

```

651  ENGHFLPPYNDELFAFWDKIDRLRLYNLRHNLSLDGGQPLHLPLFAEPVNPRL 700
      |||
650  ENGHFLPPYNDELLAFWDKIDRLRLYNLRHNLSLDGGQPLHLPLFTEPVNPR 699
      .
701  ELQVQHGPBGDGLGGSAGSAQSRQSVYRFPLVIDKARNAANSVIQFGNALE 750
      |||
700  ELQVQHAGDGLGGSAGSVQSRQSVYRFPLVIDKARNAASSVIQFGNALE 749
      .
751  NALTQKDSEAMTMLLQSQQQIVLQQTRDIQEKNLAAALQASLEATMTAKAG 800
      |||
750  NALTQKDSEAMTMLLQSQQQIVLQQTRDIQEKNLASLQASLEATMTAKAG 799
      .
801  AESRKTHFAGLADNWMSDNETASLALRTTAGIINTSSSTVPPIAITGGLDMA 850
      |
800  AKSRKTHFAGLADNWMSSHNETASLALRTTAGIINTSSSTVPPIAITGGLDMA 849
      .
851  PNIFGFVAVGGSRWGAASAAVAQGLQIAAGVMEQTANIIDISESYRRRRED 900
      |||
850  PNIFGFVAVGGSRWGAASAAVAQGLQIAAGVMEQTANIIDISESYRRRRED 899
      .
901  WLLQORDVAENEAQQLDSQIAALREQMDMARKQLALAETEQAHAQAVYELQ 950
      |||
900  WLLQORDVAENEAQQLDSQIAALREQMDMARKQLALAETEQAHAQAVYELL 949
      .
951  STRFTNQALYNWMAGRLSSLYYQMYDAALPLCLMAKQALEKEIGSDKTVG 1000
      |||
950  STRFTNQALYNWMAGRLSSLYYQMYDAALPLCLMAKQALEKEIGNDKTVG 999
      .
1001 VLSLPAWNDLYQGLLAGEALLLELQKLENLWLEEDKRGMEAVKTVSLDTL 1050
      |||
1000 IFTLPAWNDLYQGLLAGEALLLELQKLENLWLEEDKRGMEAVRTVSLDTL 1049
      .
1051 LRKTNPNSGFADLVKEALDENGKTPDPVSGVGVQLQNNIFSATLDLSVLG 1100
      ||| : ||| : |||
1050 LRKEKPESGFADLVK. . EVLDGKTPDPVSGVSVQLQNNIFSATLDLSTLG 1097
      .
1101 LDRSYNQA EKSRRIKNMSVTLPALLGPYQDIEATLSLGGETVALSHGVDD 1150
      ||| : ||| : |||
1098 LDRFYNQA EKAHRIKNLSVTLPALLGPYQDIAATLSLGGETVALSHGVDD 1147
      .
1151 SGLFITDLNDSRFLPFEGMDPLSGTLVLSIFHAGQDGDQRLLESNDVI 1200
      |||
1148 SGLFITDLNDSRFLPFEGMDPLSGTLVLSILHAGQDGDQRLLESNDVI 1197
      .
1201 FHIRYVMK* 1209
      |||
1198 FHIRYVMK* 1206

```

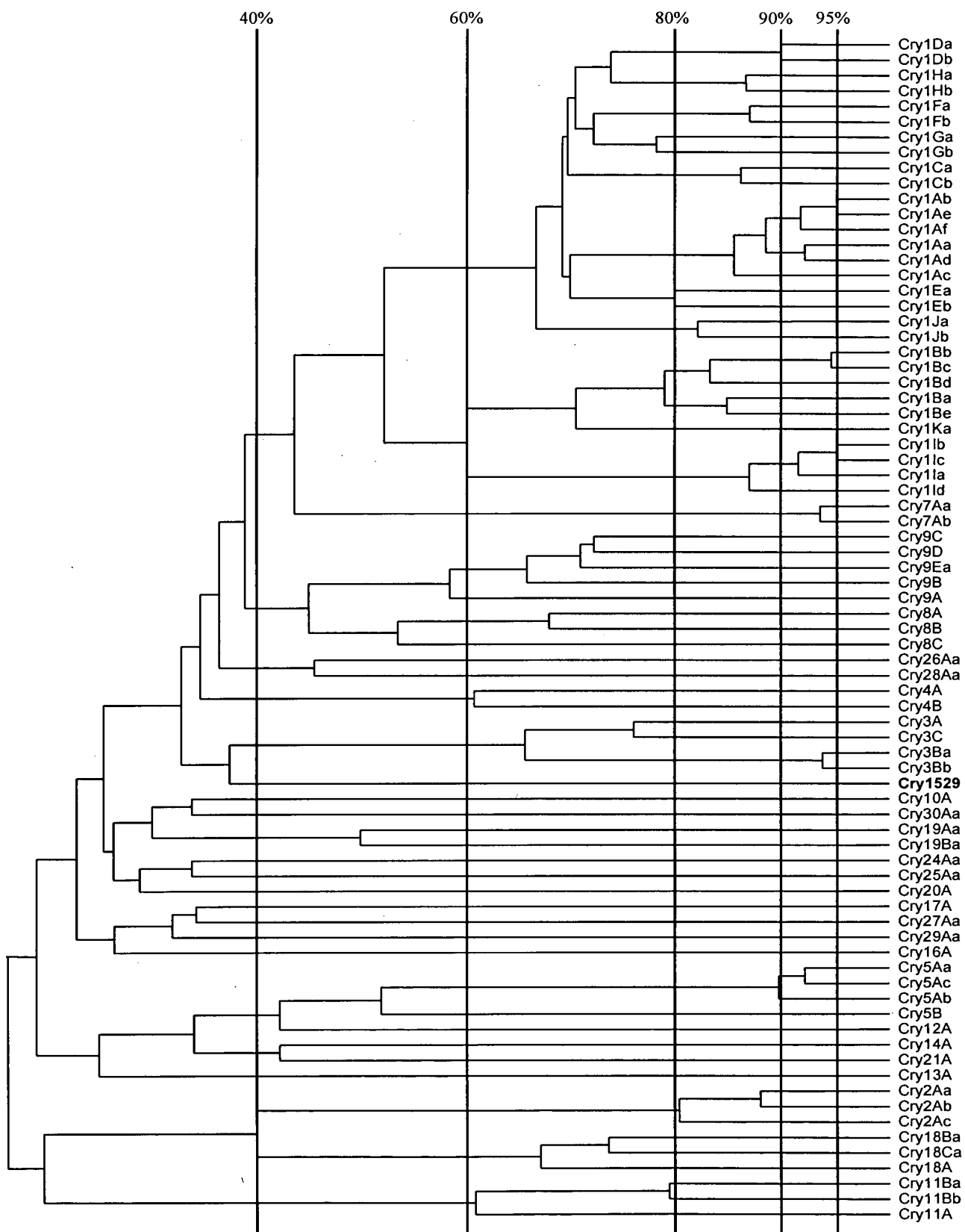



Fig. 8.

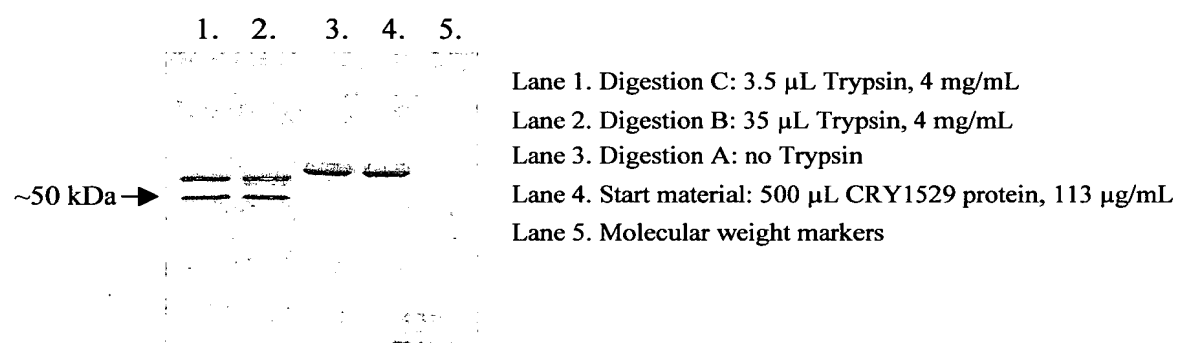


FIG. 9

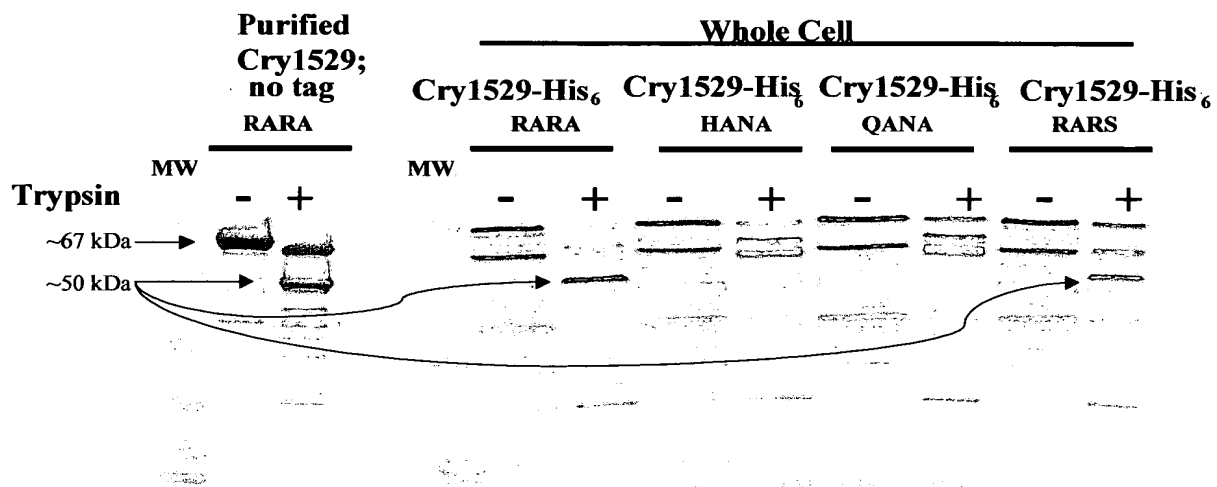


Fig. 10

		501		550
tcaA2-1529	(500)	AGTCGCTGATCCTCAATAATGACAATATGAACCGAGAGGTAT	CTTCTCTG	
tcaA1-1529	(485)	AGTCGCTGATCCTCAATAATGACAATATGAACCGTGAGGTGT	CTTCCCTG	
tcaA-W14	(485)	AGGATCTGATATTAAGCGAAACGACGATGAATAAAGAGGTCA	CTTCCCTT	
		551		600
tcaA2-1529	(550)	GATATCCTTCTGGATGTGCT	GCAGCCCGAAGGCTCTGACACGCTGACATC	
tcaA1-1529	(535)	GATATCCTGCTGGATGTGCT	GCAGTCCGAAGGCTCCGGCACACTGACATC	
tcaA-W14	(535)	GATATCTTGTTGGATGTGCT	ACAAA--AAGGCGGTAAAGATATTACTGA	
SB105				

Fig. 11A

		1901		1950
tcaA2-1529	(1824)	GATGCGCAGCACGGGTCTTTCTTTGAGCAG	TTGGATTGGCTGATTGCCA	
tcaA1-1529	(1788)	GGCGCGCAGCACGGGACTTTCTTTGAGCAG	TTGGATTGGCTGATTACCA	
tcaA-W14	(1809)	ATCATCCCAGACCGGGCTATCATTGAAGAA	TTGGACTGGCTGATTGCCA	
SB106				
		1951		2000
tcaA2-1529	(1874)	ATGCCAGCCGT	GCCGTTATCGAACACGGTGGAGAGCTTTTTCTGGATAAG	
tcaA1-1529	(1838)	ATACCAGCCGT	GCCGTAATCGAACATGGTGGAGAACTGATTCTGGATAAG	
tcaA-W14	(1859)	ATGCCAGTCGT	AGTGTGCCGGACCACCACGACAAAATTGTGCTGGATAAG	

Fig. 11B

		1651		1700
tcaB2-1529	(1611)	GGAGTGGGATGACACGTTGTCCCTGGCAACGACCGACCCGGACGAGATT		G
tcaB-W14	(1557)	CGCATGGGATACCACACAGCCC---GCCACCACTGATCCAGATGTGATC		G
tcaB1-1529	(1608)	GGAGTGGGATGACACGTTGTCCCTGGCAACGACCGACCCGGACGAGATT		G
		1701		1750
tcaB2-1529	(1661)	CGATGGCCGACCCGATGCAATACAAGCTGGC	TATATTTATT	CACACCATG
tcaB-W14	(1604)	CTATGGCGGACCCGATGCATTACAAGCTGGC	GATATTCCTGC	TACCCCTT
tcaB1-1529	(1658)	CGATGGCCGACCCGATGCAATACAAGCTGGC	TATCTTTATT	CACACCTTG

SB101

Fig. 12A

		2051		2100
tcaB2-1529	(1999)	TGGGACAAAATCGATCTGCGTTTATACAATTTG	CGCCACAATTTGAGTCT	
tcaB-W14	(1951)	TGGGATAAACTTGAGTTACGCCTATACAACCTG	CGCCACAATCTGAGTCT	
tcaB1-1529	(1996)	TGGGATAAAATCGACCTGCGTCTCTACAATTTA	CGCCACAATCTGAGCCT	
SB102				
		2101		2150
tcaB2-1529	(2049)	GGACGGTCAGCCGCT	TCATTTGCCGCTCTTTGCCGAACCGGTCAATCCGC	
tcaB-W14	(2001)	GGATGGTCAACCGCT	AAATCTGCCACTGTATGCCACGCCGGTAGACCCGA	
tcaB1-1529	(2046)	GGACGGTCAGCCGCT	TCATTTGCCGCTCTTTACCGAACCGGTCAATCCTC	

Fig. 12B

		2901		2950
tcaB2-1529	(2845)	CTGCAAAGCACCCGCTTTACGAATCAAGCTT	TGTATAACTGGATGGCTGG	
tcaB-W14	(2797)	CTGCAAACCACTCGTTTTACCGGGCAGGCAC	TGTATAACTGGATGGCCGG	
tcaB1-1529	(2842)	CTGCTAAGCACCCGTTTTACGAATCAAGCTT	TGTATAACTGGATGGCCGG	
SB103				
		2951		3000
tcaB2-1529	(2895)	ACGTCTGTC	GTCTCTATACTATCAAATGTATGACGCCGCATTGCCGCTCT	
tcaB-W14	(2847)	TCGTCTCTC	CGCGCTCTATTACCAAATGTATGATTCCACTCTGCCAATCT	
tcaB1-1529	(2892)	ACGTCTGTC	GTCTCTATACTATCAAATGTATGACGCCGCATTGCCGCTCT	

Fig. 12C

		2201		2250
tcaC-1529	(2125)	AGCTCGTTTTGGTAC	CGAAGCTCCACCCAGTATTGGCTGGATGAGAAA	CA
tcdB1-W14	(2149)	CACACCTTGCATTAC	CGTAGCTCTGTCCAGTTCTGGCTGGATGAAAAA	GC
tcdB2-W14	(2128)	CACACCTTGC GTTAC	CGCAGTTCCTCCCAATTCTGGCTGGATGAAAAA	GC
xptC1-Xwi	(2188)	ACCACGCTGTATTAT	CGCAGCTCTGCCCAGTTCTGGCTGGATGAGAAA	TT

SB215

Fig. 13A

		4501		4550
tcaC-1529	(4263)	ATGGGTTTACAGTAAACGAAGATGAAAATGATAC	CATGGACTCATCATTAT	
tcdB1-W14	(4380)	GTGGTTTACCGTGAGTGAGGATGAGAATGATAC	GGCCG-CTGATGCGCTG	
tcdB2-W14	(4362)	CTGGTTTACTGTCAATGAAGATGAAAATGACAC	AGCCG-CTGAGGTGAAG	
xptC1-Xwi	(4428)	CTGGTTTGTGGTGAATGAAGATGAAAATGACAC	TGCCG-GTGAAATGACA	

SB217

Fig. 13B

		1051		1100
tccC-1529	(1027)	TAT	CGTTATGAATATGATCCGGTAGGCAAT	ATCCTTTCTATTTACAATGA
tccC1-W14	(973)	CTA	CGCTATAAGTATGATCCGGTGGGGAAT	GTTATCAGTATCCATAATGA
tccC2-W14	(940)	TTA	CGCTATCAATATGACCCGGTAGGCAAT	GTGATCAATATCCGTAATGA
tccC3-W14	(961)	CTG	CGCTATGAATATGACCCGGTAGGCAAT	GTCATCAGCATCCGTAATGA
tccC4-W14	(961)	CTA	CGCTATGAACATGATCCTGTAGGGAAT	ATTATTAGTGTCCGTAATGA
tccC5-W14	(955)	CTA	CGCTATCAATATGACCCAGTAGGCAAT	GTCATTAGTATCCGTAATGA
xptB1-Xwi	(973)	CTG	CGTTATGAATATGATCCTGTGCGAAAT	GTGCTGAAATCAACTAATGA

SB212

Fig. 14A

		1951		2000
tccC-1529	(1903)	TACAAGACCATC	CGCTATTTCAGGCAAAGAGCGGGATG	CCACAGGCCTGTA
tccC1-W14	(1861)	TACAAATTTATT	CGTTACTCCGGTAAAGAGCGGGATG	CCACTGGATTGTA
tccC2-W14	(1807)	TATAAAACGATT	CGCTATTCCGGCAAAGAACGAGATG	CCACCGGGTTGTA
tccC3-W14	(1849)	TATAAAACTATC	CGTTATTTCAGGCAAAGAGCGGGATG	CCACCGGGCTATA
tccC4-W14	(1849)	TACAAAATCCTC	CGTTACTCAGGTAAAGAACGCGATG	CTACCGGGCTCTA
tccC5-W14	(1822)	TATAAAACCATT	CGTTATTCTGGTAAAGAGCGGGATG	TTACCGGGCTGTA
xptB1-Xwi	(1855)	TACAAAACCGTG	CGTTATTCTGGCAAAGAGCGGGATG	CAACAGGGTTGTA

SB213

Fig. 14B